

FIGURE 1A

hskca3d seq (Our sequence)
Y08263 SEQ (AAD14 sequence)
G16005 SEQ (Genomic sequence in STS database)
U69884 SEQ rat SKCa3 (old sequence)
R69884 SEQ rat SKCa3 (revised October 1997)

hSkca3 AAD14	GCCTCACACGCTCTAGAGGACCACCTCCTGAGAGAGTTCTTCACCCCTCTTCTTCTCCAAGCTCCC	70 70
hSkca3 AAD14	CTCCTGCTCTCCCTCCCTGCCAATACAATGCATTCTTGAGTGGCAGCGCTGGACTCCAGGCAGCCCCA	140 140
hSkca3 AAD14	GAGAACCGAACCAAGCCAAAGAGAGGACTGGAGCCAAGATACTGGTGGGGAGATTGCATCCCTGGCTT	210 210
hSkca3 AAD14	CTTGAGGACATCTTGGAGCGAGGTGGCTTGGGTGGGGCTTGTGCTGCAGGAATACAGCCAGGC	280 280
hSkca3 AAD14 G16005 R69884	CCCAAGATGGACACTCTGGGACTTCCATGACTCGGGGTGGGGACTTGGATGAAGACCCCAAGTGCC	350 350
	C-----G-----TC-----N-----T	23 65
Trinucleotide repeat		
hSkca3 AAD14 G16005 R69884	CCTGTCCATCCTCTGGGATGAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCCACCAACCGCC	420 420
	T-----T-----G-----AG-----AG-----AG-----AG-----AG-----AG-----AG-----	93 135
Trinucleotide repeat		
hSkca3 AAD14 G16005 R69884	AGCGTCACC AGCAGCCCCCAGCAGCCCCTGGGACCCCTCGCTGCAGCCTCAGCCTCCGAGCTTCAGCA	490 490
	T-----T-----T-----C-----T-----N-----C-----C-----C-----T-----T-----	163 205
Trinucleotide repeat		
hSkca3 AAD14 G16005 R69884	GCAG	560 560
	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	233 275
Trinucleotide repeat		
hSkca3 AAD14 G16005 R69884	TCTCAGCTGCCAACCTCCAGAGCCAGCCCGTCCACCCCTGGCCTGCTGCACCTCTCCCCA	630 630
	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	303 345

FIGURE 1B

hSkca3	CAGGGCCCCCCC	TTCGTCCAACCTCACC	GGCCATCCTCCACCC	TCCAGGCAAGGCAGCCAGCTCA		700
AAD14	-C-	-T-				700
G16005	A--NN--NC		A-NN-	-C-		373
R69884	-T--AAT-	-AG-				415
hSkca3	ATCTCA <u>AATG</u> ACCA	TGCTGGCCACTCTCA	AGTTCCACAGCTACAAGT	GGGCCTGGGGAGGCAGCCG		770
AAD14	-	-	-T-	-T-		770
G16005	-	-G-	-C-	-T-		443
R69884	-	-				485
hSkca3	GCACCGACAGGCCAG	CCCCCTGGTGACCGGCGG	ACAGCAACCC	TTCACGGAGATGCCCATGAGCTCC		840
AAD14	-	-	-	-		840
G16005	-	-	-	-		513
U69884	-	-G-	-T-	-A-T-		9
R69884	-	-G-	-	-		555
hSkca3	TGCAAGTATA	CGGTGGGT	CATGAAGCCC	TCA	GGCCCTCCGGAGGAACCTCATCGAGG	910
AAD14	-	-	-T-	-		910
G16005	-	-	-	-T-A-T-		583
U69884	-	-A-C-	-A-	-T-A-T-		79
R69884	-	-A-C-	-A-	-T-A-T-		625
hSkca3	CCGAGACTGAGGGCC	AAACCC	CTCCAGCTT	TCAGCCTAGCAACCCCC	CGGAGATCGTCATCTCC	980
AAD14	-	-	-	-		980
G16005	-	-C-	-C-T-C-	-A-TA-	-A-	653
U69884	-	-C-	-C-T-C-	-A-TA-	-A-	149
R69884	-	-	-	-		695
hSkca3	GGAGGACAACC	ATGCC	ACCAGACCC	TGCTCCATCAC	CCCTAACGCCAACACCAGCATGCC	1,050
AAD14	-	-	-	-C-C-T-	-	1,050
U69884	-	-T-	-T-	-C-C-T-	-	219
R69884	-	-	-	-		765
hSkca3	ACCACCGCCAGCAG	CACCT	CCCCAAAGCC	AAACAGCGGAAAACCAAA	ACATTGGCTATAAGCTGG	1,120
AAD14	-	-	-	-		1,120
U69884	-	-T-TG-	-	-		289
R69884	-	-T-TG-	-	-		835
hSkca3	GACACAGGAGGGCC	CT	TTGAAAAGAGAAAGCG	ACTGAGT	GACTATGCTCTGATT	1,190
AAD14	-	-G-	-	-		1,190
U69884	-	-G-	-	-		359
R69884	-	-	-	-		905
hSkca3	AATTGTTGTT	TATGGT	GATAGAGACCGAG	CTCTGGGTTG	ACTCAAGGACTCCATGTT	1,260
AAD14	-	-	-A-G-	-	-T-	1,260
U69884	-	-	-A-G-	-	-T-	429
R69884	-	-	-	-	-	975

FIGURE 1C

hSkca3	GCCCTGAAATGCCGTATCAGTCTGCCACCATCATCCTTTGGGCTTGATCATCGCCTACCACACACGTG	1,330
AAD14	-----	1,330
U69884	T-----T-A-----GC-T-T-----A-G-----	499
R69884	T-----T-A-----GC-T-T-----A-G-----	1,045
hSkca3	CAGTCCAGCTTCTCGTGTACGACAACGACGCCGATGACTGGCGGATAGCCATGACCTACGAGCGCATTCT	1,400
AAD14	-----	1,400
U69884	A---A---T---T-GT-A---T-----569	
R69884	A---A---T---T-GT-A---T-----1,115	
hSkca3	CTACATTAAGCTGGAGATGCTGGTGTACACACCAACCAATTCTGGCGAGTACAAGTTCTTCTGGCG	1,470
AAD14	-----	1,470
U69884	C-----G-G-C-T-C-----A-----A-----639	
R69884	C-----G-G-C-T-C-----A-----A-----1,185	
hSkca3	GCACGCCCTGGCCTTCCTACACACCCCTCCCCGGAGGCCGATGTGGACATCATCCTGTCTATCCCCA	1,540
AAD14	-----	1,540
U69884	C-----T-----A-----T-C-----T-T-C-----709	
R69884	C-----T-----A-----T-C-----T-T-C-----1,255	
hSkca3	TGTTCCCTGCGCCTGTACCTGATCGCCCAGTCATGCTACACAGCAAGCTTTCACCGATGCCCTCGTC	1,610
AAD14	-----	1,610
U69884	T-----A-----T-----G-----A-----779	
R69884	T-----A-----T-----G-----A-----1,325	
hSkca3	CCGCAGCATGGGGCCCTAACAAAGATCAACTAACACCCGCTTGTCAATGAAGCGCT <u>CATGACCA</u>	1,680
AAD14	-----	1,680
U69884	A-----A-C-----T-----T-----849	
R69884	A-----A-C-----T-----T-----1,395	
hSkca3	TCTGCCCTGGCACTGTGCTCGTGTTCAGCATCTCTGTGGATCATTGCTGCCCTGGACCCTCGTGT	1,750
AAD14	-----	1,750
U69884	G-----G-----AA-----C-----T-GA-A-----919	
R69884	G-----G-----G-----C-----T-GA-A-----1,465	
hSkca3	CTGTGAAAGGTACCATGACCAGCAGGACGTAACTAGTAACCTTCGGTGCATGTGGCTCATCTCCATC	1,820
AAD14	-----	1,820
U69884	-----	989
R69884	-----	1,535
hSkca3	ACATTCCTTCCATTGGTTATGGGGACATGGTCCCCACACATACTGTGGAAAGGTGTCTGTCTCCCA	1,890
AAD14	-----	1,890
U69884	G-----C-----T-----1,059	
R69884	G-----C-----T-----1,605	
hSkca3	CTGGCATCATGGGTGCAGGCTGCACGTGCCCTTGTGGTGGCCGTTGGCCGAAAGCTGGAACTCACCAA	1,960
AAD14	-----	1,960
U69884	C-----A-T-----T-G-----C-----1,129	
R69884	C-----A-T-----T-G-----C-----1,675	

FIGURE 1D

hSkca3	ACGGAGAACGTGCATAACTCATGATGGACACTCAGTCACCAAGCGGATCAAGAATGCTGCAGCA	2,030
AAD14	-----CG-----	2,030
U69884	---A-----T-----C-----A-----C-----C-----C	1,199
R69884	---A-----T-----C-----A-----C-----C-----C	1,745
hSkca3	AATGTCTTCGGAAACATGGTTAATCTATAAACACACAAAGCTGCTAAAGAAGATTGACCATGCCAAAG	2,100
U69884	-----C-----C-G-----C-----C-----C	1,269
R69884	-----C-----C-G-----C-----C-----C	1,815
hSkca3	TGAGGAAACACCAGAGGAAGTTCTCCAAGCTATCCACCAAGCTTGGAGGAGCGTCAAGATGGAACAGAGGAA	2,170
U69884	-----C-----T-----AC-----G-T-----A-----C	1,339
R69884	-----C-----T-----AC-----G-T-----A-----C	1,885
hSkca3	GCTGAGTGACCAAGCCAAACACTCTGGTGGACCTTCCAAGATGCAGAATGTATGACTTAATCACA	2,240
U69884	-----C-----C-----G-----G	1,409
R69884	-----C-----C-----G-----G	1,955
hSkca3	GAACTCAATGACCGGAGCGAAGACCTGGAGAAGCAGATTGGCAGCCTGGAGTCGAAGCTGGAGCATCTCA	2,310
U69884	-----G-----C-----T-----A-----A-----C-----C	1,479
R69884	-----G-----C-----T-----A-----A-----C-----C	2,025
hSkca3	CCGCCAGCTTCAACTCCCTGCCCTGCTCATGCCACACCCCTGCCAGCAGCAGCAGCTCCTGTC	2,380
U69884	-----A-----T-----C-----A-----A-----G-CA-	1,549
R69884	-----A-----T-----C-----A-----A-----G-CA-	2,095
hSkca3	TGCCATCATCGAGGCCGGGGTGTCAAGCGTGGCAGTGGGCACCAACCCCACACCCCAATCTCGATAAGCCC	2,450
U69884	-----T-G-G-----CA-----T-----T-----A-T-G-----G-----TCC-----T-C-GC--T	1,619
R69884	-----T-G-G-----CA-----T-----T-----A-T-G-----G-----TCC-----T-C-GC--T	2,165
hSkca3	ATGGGGTCAGCTCACCTCCTCCGACCCGTACACAAGTTCAAGCAGTTGCTAAATAAAATCTCCCCA	2,520
U69884	-----C---A-----T-----GAATTCTA-T-TTC-AG-----A-----A	1,689
R69884	-----C---A-----T-----A-----A-----A-----A	2,235
hSkca3	CTCCAGAACATTAAAAAAA	2,590
R69884	-----	2,305

FIGURE 2A

hskca3.pep (our sequence)
 u69884.pep (old rat sequence)
 r69884.pep (rat sequence revised in October 1997)
 y08263.pep (AAD14 frame 1)
 y082631.pep (AAD14 frame 2)
 yC82632.pep (AAD14 frame 3)

	Poly Q motif		
hSKCa3 R69884 AAD14 F1	MDTSGHFHDGVGDLDEDPKCPCPSSGDECQQQQQQQQQQQQQQPPPP ASPAAPQQPLGPSLQPQPPQLQQQ	S-P-V-P-L	70
	E-----	SV--VV-----	70
			70
	Poly Q motif		
hSKCa3 R69884 AAD14 F1	QQQQQQQQQQQS PHPLSQLAQLQSQPVHPGLLHSSPTAFRAPPSNSTAILHPSSRQGSQNLN	N-A-----	140
	QQQQQAPL-----P-----V-----F-----S-----	FVQLHRHPP-FLQARQPAQSQ	140
			140
	Poly Q motif		
hSKCa3 R69884 AAD14 F2	DHLLGHSPSTATSGPGGGSRHQRQASPLVHRRDSNPTEIAMSSCKYSGGVMKPLSRSASRRNLIEAET	N-L-----P	210
	V-----V-----		210
			29
	Poly Q motif		
hSKCa3 U69884 R69884 AAD14 F2	EGQPLQLESPSNPPEIVISSREDNHAHQTLLHHPNATHNHQHAGTTASSTTFPKANKRKKNQNIGYKLGHR	G-----G-----	280
	I-----I-----		99
			280
			99
	S1	S2	
hSKCa3 U69884 R69884 AAD14 F2	RALFEKRKRLSDYALIFGMFGIVVMVIETELSWGGLYSKDSMFLALKCRISLSTIILLGLIIAYHTRGVQ	L-----L-----	350
			169
			350
			169
	S3	S4	
hSKCa3 U69884 R69884 AAD14 F2	LEVIDNDADOWRIAMTYERILYISLEMVYTNTIPGEYKFFWAARLAFAFSYTPSRAEADVDIILSIPMFL	CAI-P-----T-----	420
	G-----G-----	CAI-P-----T-----	239
			420
			239
	S4	S5	
hSKCa3 U69884 R69884 AAD14 F2	RLYLIARVMLLHSKLFDAASSRSIGALNKINFNTFVUMKTLMTICPGTVLLVFSISLNIIAAWTVRVCER	M-----CH-----	490
			309
			490
			309
	P-reg	S6	
hSKCa3 U69884 R69884 AAD14 F3	YHDQQDVTSNFLGAMWLISITFLSIGYGDMVPHTYCGKGVLLTGIMGAGCTALVVAVVARKLELTKA	K-----	560
			379
			560
			102

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FIGURE 2B

hSKCa3	HVDNFMMDTQLTKRIKNAAANVLRETWLIYKHTKLLKIDHAKVRKHQRKFQAIHQRLRSVKMEQRKLSD	630
U69884	--H-----G-----	449
R69884	--H-----G-----	630
AAD14 F3	--	172
hSKCa3	QANTLVDSLXMQNVMYDLITELNRSEDLEKQIGSLESKLEHLTASFNSLPPLIADTLRQQQQQLLSAII	700
U69884	-----T-FV	519
R69884	-----T-FV	700
hSKCa3	EARGVSVAVGTTHTPISDTPIGVSSTSFFTPTSSSC	770
U69884	----I----S-A-P--S---I----EFLIF	589
R69884	----I----S-A-P--S---I-----	770

Figure 3

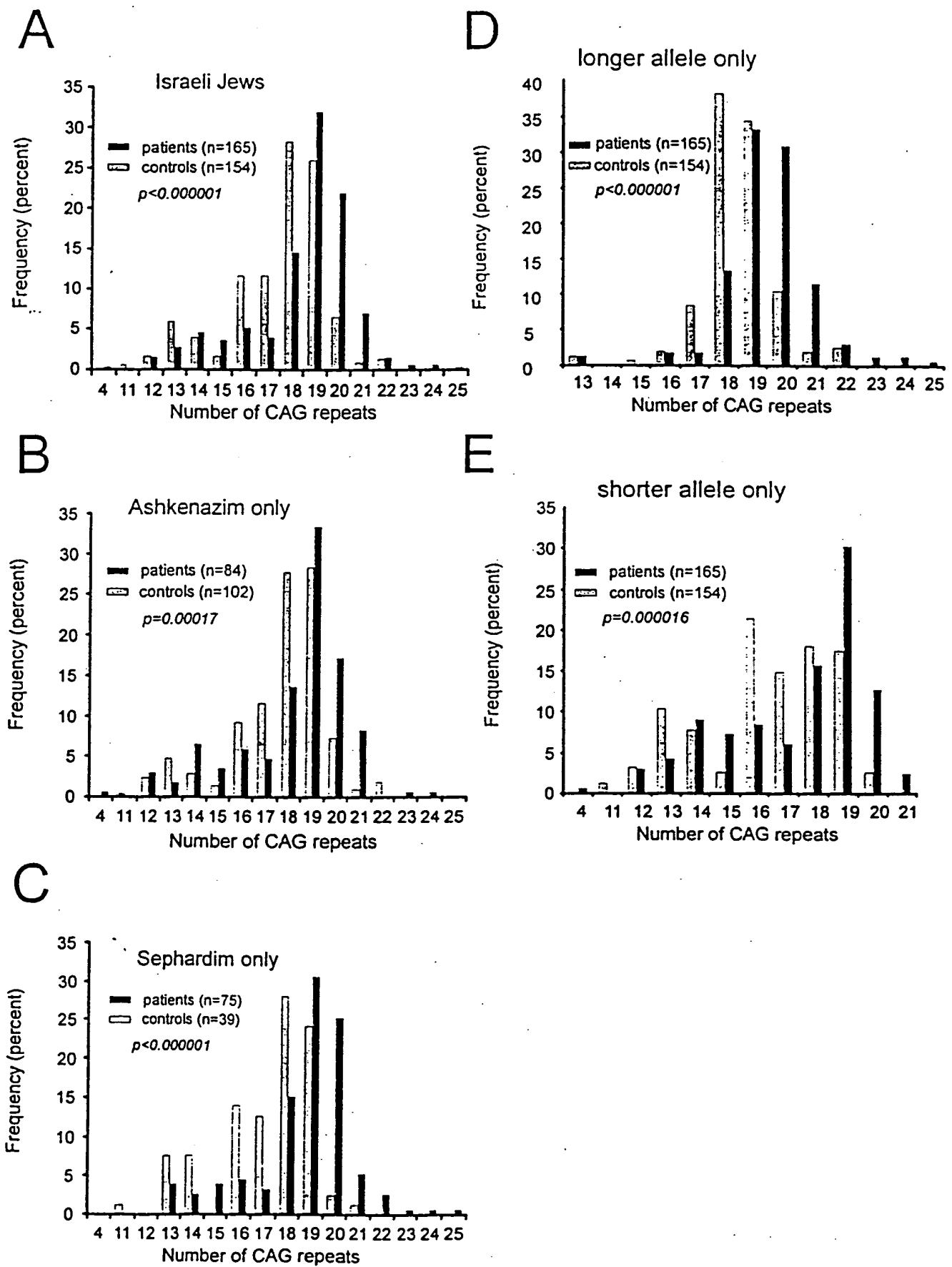


Figure 4

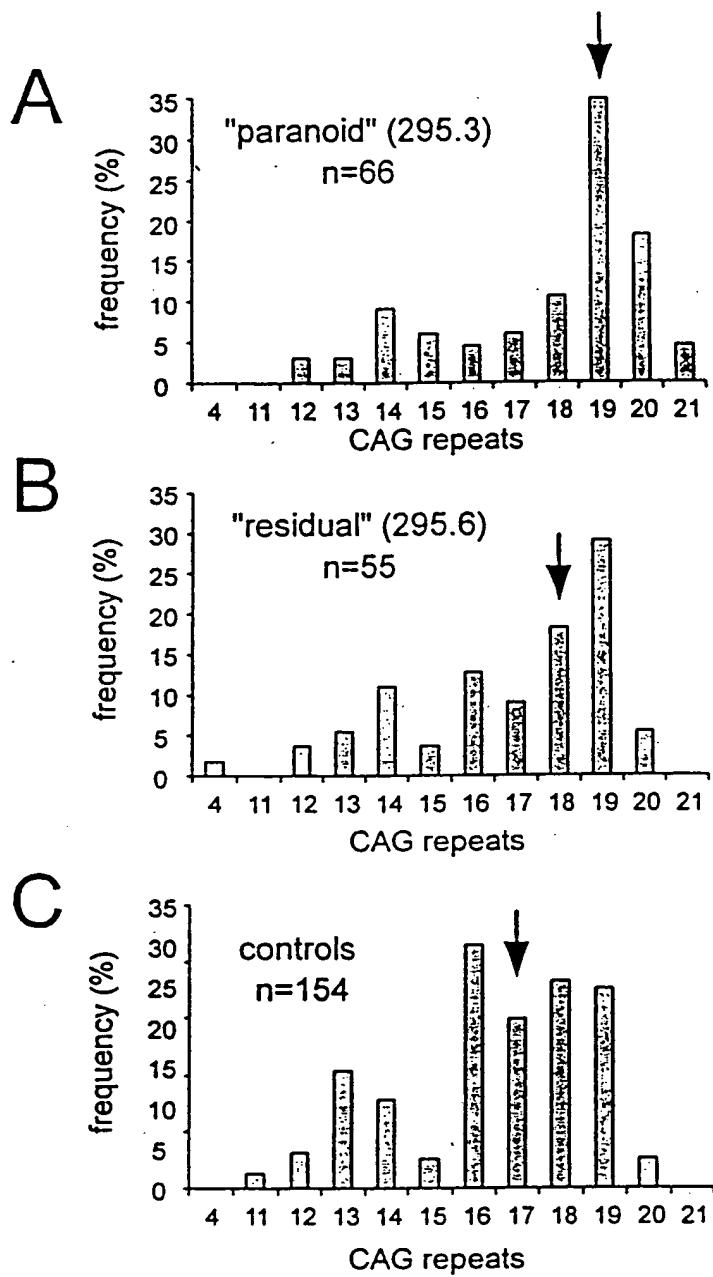


FIGURE 5A

NUCLEOTIDE SEQUENCE AND TRANSLATION OF hKCa3

-286	-280	-270	-260	-250	-240
CCCTCA	CACGCTCCTA	GAGGACCACC	TCCTGAGAGA	GTTCTTCAC	CCCCCTCTTCT
-230	-220	-210	-200	-190	-180
TTCTCCAAGC	TCCCCCTCCTG	CTCTCCCCTCC	CTGCCCAATA	CAATGCATTG	TTGAGTGGCA
-170	-160	-150	-140	-130	-120
CCGTCTGGAC	TCCAGGCAGC	CCCAGAGAAC	CGAAGCAAGC	CAAAGAGAGG	ACTGGAGCCA
-110	-100	-90	-80	-70	-60
AGATACTGGT	GGGGGAGATT	GGATGCCCTGG	CTTTCTTGA	GGACATCTT	GGAGCGAGGG
-50	-40	-30	-20	-10	
TGGCTTTGGG	GTGGGGGCTT	GTGCTGCAGG	GAATACAGCC	AGGCCCCAAG	ATG GAC ACT
					Met Asp Thr
15	30	45	60		
TCT GGG CAC TTC CAT GAC TCG GGG GTG GGG GAC TTG CAT GAA GAC CCC AAG TGC	Ser Gly His Phe His Asp Ser Gly Val Gly Asp Leu Asp Glu Asp Pro Lys Cys				
75	90	105			
CCC TGT CCA TCC TCT GGG GAT GAG CAG CAG CAG CAG CAG CAA CAG CAG	Pro Cys Pro Ser Ser Gly Asp Glu Gln Gln Gln Gln Gln Gln Gln Gln				
120	135	150	165		
CAG CAG CCA CCA CCG CCA CCG CCA GCA GCA CCC CAG CAG CCC CTG GGA CCC	Gln Gln Pro Pro Pro Ala Pro Pro Ala Ala Pro Gln Gln Gln Gln Gln Pro				
180	195	210	225		
TCG CTC CAG CCT CAG CCT CCG CAG CTT CAG CAG CAG CAG CAG CAG CAG CAG	Ser Leu Gln Pro Pro Gln Pro Pro Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln				
240	255	270			
CAG CAG CAG CAG CCA CCG CAT CCC CTG TCT CAG CTC GCC CAA CTC CAG AGC	Gln Gln Gln Gln Pro Pro His Pro Leu Ser Gln Leu Ala Gln Leu Gln Ser				
285	300	315	330		
CAG CCC GTC CAC CCT GGC CTG CTG CAC TCC TCT CCC ACC GCT TTC AGG GCC CCC	Gln Pro Val His Pro Gly Leu Leu His Ser Ser Pro Thr Ala Phe Arg Ala Pro				
345	360	375			
CCT TCG TCC AAC TCC ACC GCC ATC CTC CAC CCT TCC TCC AGG CAA GGC AGC CAG	Pro Ser Ser Asn Ser Thr Ala Ile Leu His Pro Ser Ser Arg Gln Gly Ser Gln				
390	405	420	435		
CTC AAT CTC AAT GAC CAC TTG CTT GGC CAC TCT CCA AGT TCC ACA GCT ACA AGT	Leu Asn Leu Asn Asp His Leu Leu Gly His Ser Pro Ser Ser Thr Ala Thr Ser				
450	465	480	495		
GGG CCT GGC GGA GGC AGC CGG CAC CGA CAG GCC AGC CCC CTG GTG CAC CGG CGG	Gly Pro Gly Gly Ser Arg His Arg Gln Ala Ser Pro Leu Val His Arg Arg				

FIGURE 5B

510	525	540	
GAC AGC AAC CCC TTC ACG GAG ATC GCC ATG AGC TCC TGC AAG TAT AGC GGT GGG Asp Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Lys Tyr Ser Gly Gly			
555	570	585	600
GTC ATG AAG CCC CTC AGC CGC CTC AGC GCC TCC CGG AGG AAC CTC ATC GAG GCC Val Met Lys Pro Leu Ser Arg Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala			
615	630	645	
GAG ACT GAG GGC CAA CCC CTC CAG CTT TTC AGC CCT AGC AAC CCC CCG GAG ATC Glu Thr Glu Gly Gln Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile			
660	675	690	705
GTC ATC TCC TCC CGG GAG GAC AAC CAT GCC CAC CAG ACC CTG CTC CAT CAC CCT Val Ile Ser Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro			
720	735	750	765
AAT GCC ACC CAC AAC CAC CAG CAT GCC GGC ACC GCC GCC ACC ACC ACC ACC TTC Asn Ala Thr His Asn His Gln Ala Gly Thr Ala Ala Ser Ser Thr Thr Phe			
780	795	810	
CCC AAA GCC AAC AAG CGG AAA AAC CAG AAC ATT GGC TAT AAC CTC CGA CAC AGG Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg			
825	840	855	870
AGG GCC CCG TTT GAA AAG AGA AAG CGA CTG AGT GAC TAT CCT CTG ATT TTT GGG Arg Ala Pro Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly			
885	900	915	
ATG TTT GGA ATT GTT GTT ATG GTG ATA GAG ACC GAG CTC TCT TGG GGT TTG TAC Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Leu Tyr			
930	945	960	975
TCA AAG GAC TCC ATG TTT TCG TTG GCC CTG AAA TGC CTT ATC AGT CTG TCC ACC Ser Lys Asp Ser Met Phe Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu Ser Thr			
990	1005	1020	1035
ATC ATC CTT TTG GGC TTG ATC ATC GCC TAC CAC ACA CGT GAA GCC CAG CTC TTC Ile Ile Leu Leu Gly Leu Ile Ala Tyr His Thr Arg Glu Ala Gln Leu Phe			
1050	1065	1080	
GTG ATC GAC AAT GGC GCG GAT GAC TGG CGG ATA GCC ATG ACC TAC GAG CGC ATC Val Ile Asp Asn Gly Ala Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile			
1095	1110	1125	1140
CTG TAC ATC AGC CTG GAG ATG CTG GTG TGC GCC ATC CAC CCC ATT CCT GGC GAG Leu Tyr Ile Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu			
1155	1170	1185	
TAC AAG TTC TTC TGG ACG GCT CGC CTG GCC TTC TCC TAC ACA CCC TCC CGG GCG Tyr Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg Ala			

FIGURE 5C

1200 1215 1230 1245
 GAG GCC GAT GTG GAC ATC ATC CTG TCT ATC CCC ATG TTC CTG CCC CTG TAC CTG
 Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu

 1260 1275 1290 1305
 ATC GCC CGA CTC ATG CTG CTG CAC AGC AAG CTC TTC ACC GAT GCC TCG TCC CGC
 Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg

 1320 1335 1350 ¹³⁵⁰
 AGC ATC GGG GCC CTC AAC AAG ATC AAC ACC CGC TTT GTC ATG AAG ACG
 Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr

 1365 1380 1395 1410
 CTC ATG ACC ATC TGC CCT GGC ACT GTG CTG CTC GTG TTC AGC ATC TCT CTG TGG
 Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp

 1425 1440 1455 ¹⁴⁵⁵
 ATC ATT GCT CCC TGG ACC GTC CGT CCC TGT GAA AGG TAC CAT GAC CAG CAG GAC
 Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His Asp Gln Gln Asp

 1470 1485 1500 1515
 GTA ACT AGT AAC TTT CTG CCT GCC ATG TGG CTC ATC TCC ATC ACA TTC CTT TCC
 Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ser Ile Thr Phe Leu Ser

 1530 1545 1560 1575
 ATT GGT TAT GGG GAC ATG GTG CCC CAC ACA TAC TGT CGG AAA GGT GTC TGT CTC
 Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu

 1590 1605 1620 ¹⁶²⁰
 CTC ACT GCC ATC ATG GGT GCA GGC TGC ACT GCC CTT GTG GTG GCC GTG GTG GCC
 Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Ala

 1635 1650 1665 1680
 CGA AAG CTG GAA CTC ACC AAA GCG GAG AAG CAC GTT CAT AAC TTC ATG ATG GAC
 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp

 1695 1710 1725 ¹⁷²⁵
 ACT CAG CTC ACC AAG CGG ATC AAG AAT GCT GCA GCC AAT GTC CTT CGG GAA ACA
 Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Asn Val Leu Arg Glu Thr

 1740 1755 1770 1785
 TGG TTA ATC TAT AAA CAC ACA AAG CTG CTA AAG AAG ATT GAC CAT GCC AAA GTG
 Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Ile Asp His Ala Lys Val

 1800 1815 1830 1845
 ACG AAA CAC CAG AGG AAG TTC CTC CAA GCT ATC CAC CAG TTG AGG AGC GTC AAG
 Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser Val Lys

 1860 1875 1890 ¹⁸⁹⁰
 ATG CAA CAG AGG AAC CTG AGT GAC CAA GCC AAC ACT CTG GTG GAC CTT TCC AAG
 Met Glu Gln Arg Lys Leu Ser Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys

FIGURE 5D

1905	1920	1935	1950
ATG CAG AAT GTC ATG TAT GAC TTA ATC ACA GAA CTC AAT GAC CGG AGC GAA GAC Met Gln Asn Val Met Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp			
1965	1980	1995	
CTG GAG AAG CAG ATT GGC AGC CTG GAG TCG AAG CTG GAG CAT CTC ACC GCC AGC Leu Glu Lys Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser			
2010	2025	2040	2055
TTC AAC TCC CTG CCG CTG CTC ATC GCC GAC ACC CTG CGC CAG CAG CAG CAG CAG Phe Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln			
2070	2085	2100	2115
CTC CTG TCT GCC ATC ATC GAG CCC CGG CGT GTC AGC GTC GCA CTG GCC ACC ACC Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val Gly Thr Thr			
2130	2145	2160	
CAC ACC CCA ATC TCC GAT AGC CCC ATT GGG GTC AGC TCC ACC TCC TTC CCG ACC His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser Thr Ser Phe Pro Thr			
2175	2190	2205	2220
CCG TAC ACA AGT TCA AGC AGT TGC TAA ATA AAT CTC CCC ACT CCA GAA CCA TTA Pro Tyr Thr Ser Ser Ser Ser Cys *			
2235			
AAA AAA AAA AAA			

FIGURE 6

Alignment of cDNA and Genomic sequence of hCa3
showing intron/exon boundary

	1140	1150	1160	1170	1180	1190
hCa3f.seq	ACTGAGTGACTATGCTCTGATTTGGGATGTTGGAATTGTGTTATGGTGATA	GAGA				
B1-1395.SEQ	ACTGAGTGACTATGCTCTGATTTGGGATGTTGGAATTGTGTTATGGTGATA	GAGA				
	1200	1210	1220	1230	1240	1250
hCa32f.seq	CCGAGCTCTCTGGGGTTGTACTCAAAGGACTCCATGTTCGTTGCCCTGAAATGCC					
B1-1395.SEQ	CCGAGCTCTCTGGGGTTGTACTCAAAGGTAGGGCCTGTGGTTCTCTTACCTTGA					
				↑ begin Intron 1		
B1-1395.SEQ	ACAAAAGGAATATGTAGGTAGCAAGAGAGGGATTGAGAGAGGGGGATATTGAGAGAGAGA					
B1-1395.SEQ	GAGAGAGAGAGAGAGAGATTGAGAGATTGGGAGGGAGACTGGGAGAGAGAGGGTGG					
B1-1395.SEQ	TGGTGGTGAGAGGCCTGCTCAGTTATAT					

FIGURE 7

Genomic map of hKCa3, first exon

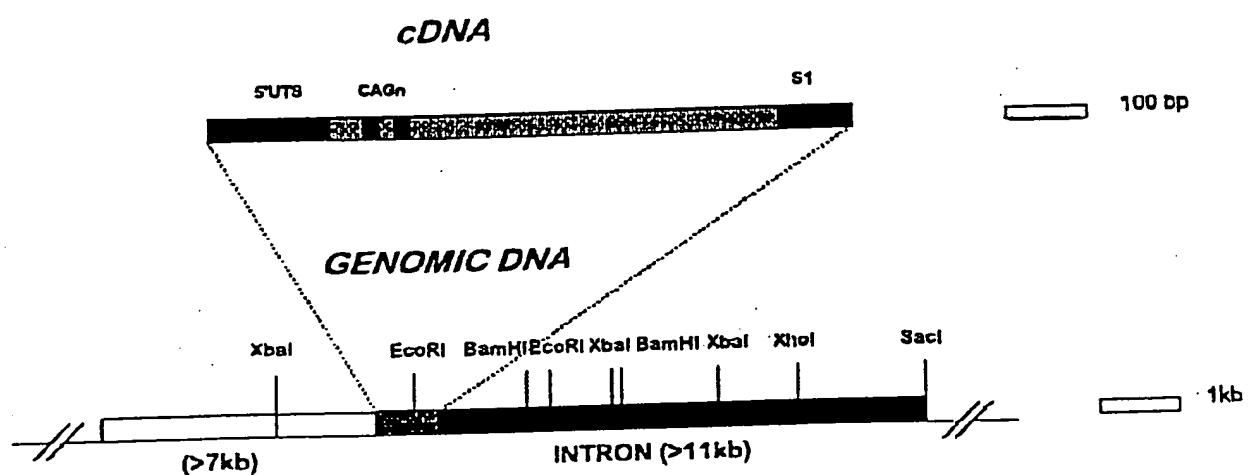


FIGURE 8

5' Flanking/Untranslated sequence of hKCa3/KCNN3

CCC TTG AAC ACG AGG CGT TAG ACA CTC CAG TCC ATG	36
GTA GGT TAG TTT TTA TCC NCC GGG GTG TTA GAA ACG	72
TGG GNA TCC CCC CCT GGT TCT GTG ACC TTT GAC GTT	108
GTT ACT CAA CAC CTT TTA AGC ATC AGG CTT TGT AAA	144
TTG AGA CCA TAC TGG CCC ACC TCC TTG GGT GTT TGA	180
AGA CTG TAT CCG GAT AAT ATA TGT GAA ACN ACC TAT	216
CGT AAA CCC TGG TGG TTA ATA AAT GTT TGC CTT CCC	252
CTC CGT CTG CCC CCT TCA TCC AGG GTG CAC ACC TCC	288
CCT CCT TCG GAG GCC CTC TGT CCC TCC TCC CCA TCG	324
CCC AGC GTG AGC GAA CAT CCC TTA TCG CCG TGG GCT	360
TAA GGG TTG TGG CCA TAC CTG TCA GAG GAA AGA GGA	396
CAG CGG CTC AGC TCC GGG GTG GGG GAG CAA AAA CTA	432
CAG TTC CCA GTC CTC GCT GCG CCG CCA CTG GGG CCG	468
GAG CCC AGG ACG CCA GGC CCC TCC TCT GGG GAG GAG	504
CCT ATG CGG GGG GCG GAG CTA GGA GGA GGT TGG AGA	540
GTT AAG CCA AGC CAA TGA GAC CAG CTG CTA ATA AGT	576
GGG CTT GGC TTA CAA TGT AAC AGT GGC AGG AGG AGG	612
CGA GCG AAG CTA TTG AGC CAG CGA GGA GTG AAG TGA	648
GCC TGG CCT CAC ACG CTC CTA GAG GAC CAC	684

↑
start of overlap with HSKCa3 cDNA sequence